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1 .....GCGA 4  
1 CTCGGGTAACCTTCTTGAGCGCGGCCACAGCAGCCTTGATCATGAAGGCGA 50  
5 GCATGGTGACCTTGACGCCGCTCTTTTCGTTCTCTTTGTTGAACTGCACG 54  
51 GCATGGTGACCTTGACGCCGCTCTTTTCGTTCTCTTTGTTGAACTGCACG 100  
55 CGAAAGGCTTCCAGGTCGGTGATGTCCGCGTCGTCGTGGTTGGTGACGTG 104  
101 CGAAAGGCTTCCAGGTCGGTGATGTCCGCGTCGTCGTGGTTGGTGACGTG 150  
105 CGGGATGACCACCCAGTTGCGGTGCAGGTTTTTCGATGGCATAATATCTG 154  
151 CGGGATGACCACCCAGTTGCGGTGCAGGTTTTTCGATGGCATAATATCTG 200  
155 CGTTGCGACGTGTAACACACTATTGGAGACATATCATGCAAACGCTCAGC 204  
201 CGTTGCGACGTGTAACACACTATTGGAGACATATCATGCAAACGCTCAGC 250  
205 ATCCAGCACGGTACCCTCGTCACGATGGATCAGTACCGCAGAGTCCTTGG 254  
251 ATCCAGCACGGTACCCTCGTCACGATGGATCAGTACCGCAGAGTCCTTGG 300  
255 GGATAGCTGGGTTCACGTGCAGGATGGACGGATCGTCGCGCTCGGAGTGC 304  
301 GGATAGCTGGGTTCACGTGCAGGATGGACGGATCGTCGCGCTCGGAGTGC 350  
305 ACGCCGAGTCGGTGCCTCCGCCAGCGGATCGGGTGATCGATGCACGCGGC 354  
351 ACGCCGAGTCGGTGCCTCCGCCAGCGGATCGGGTGATCGATGCACGCGGC 400  
355 AAGGTCGTGTTACCCGGTTTCATCAATGCCACACCCATGTGAACCAGAT 404  
401 AAGGTCGTGTTACCCGGTTTCATCAATGCCACACCCATGTGAACCAGAT 450  
405 CCTCCTGCGCGGAGGGCCCTCGCACGGGCGTCAATTCTATGACTGGCTGT 454  
451 CCTCCTGCGCGGAGGGCCCTCGCACGGACGTCAATTCTATGACTGGCTGT 500  
455 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTAGCG 504  
501 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTAGCG 550  
505 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 554  
551 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 600  
555 GATCAACGAAAACGCCGATTTCGGCCATCTACCCAGGCAACATCGAGGCCG 604  
601 GATCAACGAAAACGCCGATTTCGGCCATCTACCCAGGCAACATCGAGGCCG 650

Fig. 1A

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605 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCCGCATG 654  
|||||  
651 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCCGCATG 700  
|||||  
655 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 704  
|||||  
701 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 750  
|||||  
705 GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGAGGGAACGGCTG 754  
|||||  
751 GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGAGGGAACGGCTG 800  
|||||  
755 TGGCCAAAGATCGGATCACAGCCCTGTCAGATCAGTATCATGGCACGGCA 804  
|||||  
801 TGGCCAAAGATCGGATCACAGCCCTGTCAGATCAGTATCATGGCACGGCA 850  
|||||  
805 GGAGGTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 854  
|||||  
851 GGAGGTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 900  
|||||  
855 AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCCGTGATCGGGCGGTAA 904  
|||||  
901 AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCCGTGATCGGGCGGTAA 950  
|||||  
905 TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTCATGGG 954  
|||||  
951 TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTCATGGG 1000  
|||||  
955 ATGAGTCCCGCCGAGTACATGGAGTGTTACGGACTCTTGGATGAGCGTCT 1004  
|||||  
1001 ATGAGTCCCGCCGAGTACATGGAGTGTTACGGACTCTTGGATGAGCGTCT 1050  
|||||  
1005 GCAGGTCGCGCATTGCGTGTACTIONTACCAGGAAAGGATGTTCCGGCTGCTGC 1054  
|||||  
1051 GCAGGTCGCGCATTGCGTGTACTIONTACCAGGAAAGGATGTTCCGGCTGCTGC 1100  
|||||  
1055 ACCGCCACAATGTGAAGGTCGCGTCGCAGGTTGTGAGCAATGCCTACCTC 1104  
|||||  
1101 ACCGCCACAATGTGAAGGTCGCGTCGCAGGTTGTGAGCAATGCCTACCTC 1150  
|||||  
1105 GGCTCAGGGGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 1154  
|||||  
1151 GGCTCAGGGGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 1200  
|||||  
1155 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGTAACATGATCG 1204  
|||||  
1201 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGTAACATGATCG 1250  
|||||  
1205 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 1254  
|||||  
1251 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 1300  
|||||

Fig 1B

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1255 GACGTGCTGACCCAGAGAAGATTCTTGAAATGGCGACGATCGATGGGGC 1304  
|||||  
1301 GACGTGCTGACCCAGAGAAGATTCTTGAAATGGCGACGATCGATGGGGC 1350  
  
1305 GCGTTCGTTGGGAATGGACCACGAGATTGGTTCCATCGAAACCGGCAAGC 1354  
|||||  
1351 GCGTTCGTTGGGAATGGACCACGAGATTGGTTCCATCGAAACCGGCAAGC 1400  
  
1355 GCGCGGACCTTATCCTGCTTGACCTGCGTCACTCAGACGACTCTCAC 1404  
|||||  
1401 GCGCGGACCTTATCCTGCTTGACCTGCGTCACTCAGACGACTCTCA 1447  
  
1405 CATCATTTGGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGGA 1454  
|||||  
1448 CATCATTTGGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGGA 1497  
  
1455 CACTGTCCTGATTGACGGAACGTTGTGATGGAGAACCGCCGCTTGAGCT 1504  
|||||  
1498 CACTGTCCTGATTGACGGAACGTTGTGATGGAGAACCGCCGCTTGAGCT 1547  
  
1505 TTCTTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGC 1554  
|||||  
1548 TTCTTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGC 1597  
  
1555 GCCACAGCTATTTTGCAGCGGGCGAACATGGTGGCTAACCAGCTTGCGG 1604  
|||||  
1598 GCCACAGCTATTTTGCAGCGGGCGAACATGGTGGCTAACCAGCTTGCGG 1647  
  
1605 CAGCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAA 1654  
|||||  
1648 CAGCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAA 1697  
  
1655 TCGCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGAT 1704  
|||||  
1698 TCGCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGAT 1747  
  
1705 GGATACAGAATTGCCATGAATGCGGCACTTCGTCCTTCGCTCGTGTGGA 1754  
|||||  
1748 GGATACAGAATTGCCATGAATGCGGCACTTCGTCCTTCGCTCGTGTGGA 1797  
  
1755 ATCGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGTG 1804  
|||||  
1798 ATCGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGTG 1847  
  
1805 AAAG..... 1808  
|||||  
1848 AAAGCCCCGAG 1858

Fig. 1C

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1 .....GAGCGCGGCCACAGCAGCCTTGATCATGAAGGCGA 35  
1 CTCGGGTAACCTTCTTGAGCGCGGCCACAGCAGCCTTGATCATGAAGGCGA 50  
36 GCATGGTGACCTTGACGCCGCTCTTTTCGTTCTCTTTGTTGAACTGCACG 85  
51 GCATGGTGACCTTGACGCCGCTCTTTTCGTTCTCTTTGTTGAACTGCACG 100  
86 CGAAAGGCTTCCAGGTCGGTGATGTCCGCGTCGTGGTTGGTGACGTG 135  
101 CGAAAGGCTTCCAGGTCGGTGATGTCCGCGTCGTGGTTGGTGACGTG 150  
136 CGGGATGACCACCCAGTTGCGGTGCAGGTTTTTCGATGGCGTAATATCTG 185  
151 CGGGATGACCACCCAGTTGCGGTGCAGGTTTTTCGATGGCGTAATATCTG 200  
186 CGTTGCGACGTGTAACACACTATTGGAGACATATCATGCAAACGCTCAGC 235  
201 CGTTGCGACGTGTAACACACTATTGGAGACATATCATGCAAACGCTCAGC 250  
236 ATCCAGCACGGTACCCTCGTCACGATGGATCAGTACCGCAGAGTCCTTGG 285  
251 ATCCAGCACGGTACCCTCGTCACGATGGATCAGTACCGCAGAGTCCTTGG 300  
286 GGATAGCTGGGTTACAGTGCAGGATGGACGGATCGTCGCGCTCGGAGTGC 335  
301 GGATAGCTGGGTTACAGTGCAGGATGGACGGATCGTCGCGCTCGGAGTGC 350  
336 ACGCCGAGTCGGTGCCTCCGCCAGCGGATCGGGTGATCGATGCACGCGGC 385  
351 ACGCCGAGTCGGTGCCTCCGCCAGCGGATCGGGTGATCGATGCACGCGGC 400  
386 AAGGTCGTGTTACCCGGTTTCATCAATGCCACACCCATGTGAACCAGAT 435  
401 AAGGTCGTGTTACCCGGTTTCATCAATGCCACACCCATGTGAACCAGAT 450  
436 CCTCCTGCGCGGAGGGCCCTCGCACGGCGTCAATTCTATGACTGGCTGT 485  
451 CCTCCTGCGCGGAGGGCCCTCGCACGGACGTCAATTCTATGACTGGCTGT 500  
486 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTAGCG 535  
501 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTAGCG 550  
536 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 585  
551 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 600  
586 GATCAACGAAAACGCCGATTTCGGCCATCTACCCAGGCAACATCGAGGCCG 635  
601 GATCAACGAAAACGCCGATTTCGGCCATCTACCCAGGCAACATCGAGGCCG 650

Fig. 2A

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636 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCGCATG 685  
|||||  
651 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCGCATG 700  
686 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 735  
|||||  
701 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 750  
736 GGCTCGCTCTCCCAAGTCGAACTGTGCTCGATCATGGAGGAAACGGCTG 785  
|||||  
751 GGCTCGCTCTCCCAAGTCGAACTGTGCTCGATCATGGAGGAAACGGCTG 800  
786 TGGCCAAAGATCGGATCACAGCCCTGTCAGATCAGTATCATGGCACGGCA 835  
|||||  
801 TGGCCAAAGATCGGATCACAGCCCTGTCAGATCAGTATCATGGCACGGCA 850  
836 GGAGGTCGTATATCAGTTTGGCCCCTCCTGCCACTACCACGGCGGTGAC 885  
|||||  
851 GGAGGTCGTATATCAGTTTGGCCCCTCCTGCCACTACCACGGCGGTGAC 900  
886 AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCGTGATCGGGCGGTAA 935  
|||||  
901 AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCGTGATCGGGCGGTAA 950  
936 TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTCATGGG 985  
|||||  
951 TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTCATGGG 1000  
986 ATGAGTCCCGCCGATTACATGGAGTGTTACGGACTCTTGGATGAGCGTCT 1035  
|||||  
1001 ATGAGTCCCGCCGATTACATGGAGTGTTACGGACTCTTGGATGAGCGTCT 1050  
1036 GCAGGTCGCGCATTGCGTGTACTTTGACCGGAAGGATGTTTCGGCTGCTGC 1085  
|||||  
1051 GCAGGTCGCGCATTGCGTGTACTTTGACCGGAAGGATGTTTCGGCTGCTGC 1100  
1086 ACCGCCACAATGTGAAGGTCGCGTCGAGGTTGTGAGCAATGCCTACCTC 1135  
|||||  
1101 ACCGCCACAATGTGAAGGTCGCGTCGAGGTTGTGAGCAATGCCTACCTC 1150  
1136 GGCTCAGGGGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 1185  
|||||  
1151 GGCTCAGGGGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 1200  
1186 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGTAAACATGATCG 1235  
|||||  
1201 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGTAAACATGATCG 1250  
1236 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 1285  
|||||  
1251 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 1300

Fig. 2B

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1286 GACGTGCTGACCCCAGAGAAGATTCTTGAAATGGCGACGATCGATGGGGC 1335  
|||||  
1301 GACGTGCTGACCCCAGAGAAGATTCTTGAAATGGCGACGATCGATGGGGC 1350  
|||||  
1336 GCGTTCGTTGGGSAATGGACCACGAGATTGGTTCCATCGAAACCGGCAAGC 1385  
|||||  
1351 GCGTTCGTTGGGAATGGACCACGAGATTGGTTCCATCGAAACCGGCAAGC 1400  
|||||  
1386 GCGCGGACCTTATCCTGCTTGACCTGCGTCAACCTCAGACGACTCCTCAC 1435  
|||||  
1401 GCGCGGACCTTATCCTGCTTGACCTGCGTCAACCTCAGACGACTCCTCA 1447  
|||||  
1436 CATCATTTGGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGGA 1485  
|||||  
1448 CATCATTTGGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGGA 1497  
|||||  
1486 CACTGTCCTGATTGACGGAACGTTGTGATGGAGAACCGCCGCTTGAGCT 1535  
|||||  
1498 CACTGTCCTGATTGACGGAACGTTGTGATGGAGAACCGCCGCTTGAGCT 1547  
|||||  
1536 TTCTTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGC 1585  
|||||  
1548 TTCTTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGC 1597  
|||||  
1586 GCCACAGCTATTTTGCAGCGGGCGAACATGGTGGCTAACCCAGCTTGGCG 1635  
|||||  
1598 GCCACAGCTATTTTGCAGCGGGCGAACATGGTGGCTAACCCAGCTTGGCG 1647  
|||||  
1636 CAGCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAA 1685  
|||||  
1648 CAGCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAA 1697  
|||||  
1686 TCGCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGAT 1735  
|||||  
1698 TCGCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGAT 1747  
|||||  
1736 GGATACAGAAATGCCATGAATGCGGCACTTCCGTCCTTCGCTCGTGTGGA 1785  
|||||  
1748 GGATACAGAAATGCCATGAATGCGGCACTTCCGTCCTTCGCTCGTGTGGA 1797  
|||||  
1786 ATCGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAACTG 1835  
|||||  
1798 ATCGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAACTG 1847  
|||||  
1836 AAAGGCCCCGAG 1846  
|||||  
1848 AAAGGCCCCGAG 1858

Fig. 2C

Fig. 3

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```

1 . . . . . SAATAALIMKASMTLTPLFSFSLNCTRKASRSVMSASSWLVT 45
   ||||||||||||||||||||||||||||||||||||||||||||
1 SGNFLSAATAALIMKASMTLTPLFSFSLNCTRKASRSVMSASSWLVT 50

46 GMTTQLRCRFFDGMISALRRVTHYWRHIMQTLSIQHGLVTMDQYRRVLG 95
   |||||||||||||||:||||||||||||||||||||||||||
51 GMTTQLRCRFFDGMISALRRVTHYWRHIMQTLSIQHGLVTMDQYRRVLG 100
   . . . . . START . . . . .

96 DSWVHVQDGRIVALGVHAESVPPPADRVIDARGKVVLPGFINAHTHVNQI 145
   ||||||||||||||||||||||||||||||||||||||||||||
101 DSWVHVQDGRIVALGVHAESVPPPADRVIDARGKVVLPGFINAHTHVNQI 150

146 LLRGGPSHGRQFYDWLFNVVYPGQKAMPEDVAVAVRLYCAEAVRSGITT 195
   ||||||||||||||||||||||||||||||||||||||||||||
151 LLRGGPSHGRQFYDWLFNVVYPGQKAMPEDVAVAVRLYCAEAVRSGITT 200

196 INENADSAIYPGNIEAAMAVYGEVGVVVYARMFFDRMDGRIQGYVDALK 245
   ||||||||||||||||||||||||||||||||||||||||||||
201 INENADSAIYPGNIEAAMAVYGEVGVVVYARMFFDRMDGRIQGYVDALK 250

246 ARSPQVELCSIMEETAVAKDRITALSDQYHG TAGGRISVWPAPATTTAVT 295
   ||||||||||||||||||||||||||||||||||||||||||||
251 ARSPQVELCSIMEETAVAKDRITALSDQYHG TAGGRISVWPAPATTTAVT 300

296 VEGMRWAQAFARDRAVMWTLHMAESDHDERIHGMSPADYMECYGLLDERL 345
   |||||||||||||||||||||||||||||||||||:||||||
301 VEGMRWAQAFARDRAVMWTLHMAESDHDERIHGMSPA EYMECYGLLDERL 350

346 QVAHCVYFDRKDVRLLRHNVKVASQVVS NAYLGSGVAPVPEMVERGMAV 395
   ||||||||||||||||||||||||||||||||||||||||||||
351 QVAHCVYFDRKDVRLLRHNVKVASQVVS NAYLGSGVAPVPEMVERGMAV 400

396 GIGTDNGNSNDSVNMIGDMKFMAHIHRAVHRDADVLTPEKILEMATIDGA 445
   |||||||||||:||||||||||||||||||||||||||||||
401 GIGTDNGNSNDSANMIGDMKFMAHIHRAVHRDADVLTPEKILEMATIDGA 450

446 RSLGMDHEIGSIETGKRADLILLDLRHPQTTPHHHLAATIVFQAYGNEVD 495
   |||||||||||||||||||:||||||||||||||||||||||
451 RSLGMDHEIGSIETGKRADLILLDLRH LRRLS.HHLAATIVFQAYGNEVD 499

496 TVLIDGNVVMENRRLSFLPPERELAFLEEAQSRATAILQRANMVANPAWR 545
   ||||||||||||||||||||||||||||||||||||||||||||
500 TVLIDGNVVMENRRLSFLPPERELAFLEEAQSRATAILQRANMVANPAWR 549
   . . . . . STOP . . . . .

546 SI*EMTPLLHPPPLEEIAAILARLGLGGGHDLDGYRIAMNAALPSFARVE 595
   ||||||||||||||||||||||||||||||||||||||||||||
550 SI*EMTPLLHPPPLEEIAAILARLGLGGGHDLDGYRIAMNAALPSFARVE 599

596 SLVGEGRRLRAPASRRSERPE 615
   |||||||||||:||||||
600 SLVGEGRRLRAPASRRGERPE 619

```

Fig. 4



Fig. 5A

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1 ...CCTGCGCGGAGGGCCCTCGCACGGGCGTCAATTCTATGACTGGCTGT 47  
 451 CCTCCTGCGCGGAGGGCCCTCGCACGGACGTCAATTCTATGACTGGCTGT 500  
 48 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTANCG 97  
 501 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTAGCG 550  
 98 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 147  
 551 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 600  
 148 GATCAACGAAAACNCCGATTCTGGCCATCTACCCAGGCAACATCGAGGCCG 197  
 601 GATCAACGAAAACGCCGATTCTGGCCATCTACCCAGGCAACATCGAGGCCG 650  
 198 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCGCATG 247  
 651 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCGCATG 700  
 248 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 297  
 701 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 750  
 298 GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGANGAAACNGCTG 347  
 751 GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGAGGAAACGGCTG 800  
 348 TGGCCAAAGATCGGATCACANCCCTGTANATCANTATCATGGCACNGCA 397  
 801 TGGCCAAAGATCGGATCACAGCCCTGTGAGATCAGTATCATGGCACGGCA 850  
 398 NGAGGTCCTATATCANTTTGGCCCGCTCCTGCCACTACCACNGCGGTGAC 447  
 851 GGAGGTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 900  
 448 ATTTAAANGAATCCATGGGCCA...ACCTCCCCCGTGATCCGGCGGTAA 493  
 901 ACTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCGTGATCGGGCGGTAA 950  
 494 TGTGAC..... 499  
 951 TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTCATGGG 1000

Fig. 5B

```

360 .....TNGCAGGTTGTGAGCA..TGCTACTTC 336
      |:||||||||||||| |||||
1101 ACCGCCACAATGTGAAGGTCGCGTCGCAGGTTGTGAGCAATGCCTACCTC 1150

      .
335 GGTTCAGGNGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 286
      || |||||:|||||||||||||||||||||||||||||||||||||
1151 GGCTCAGGGGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 1200

      .
285 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGTAAACATGATCG 236
      |||||||||||||||||||||||||||||||||||||||
1201 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGCAAACATGATCG 1250

      .
235 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 186
      |||||||||||||||||||||||||||||||||||
1251 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 1300

      .
185 GACGTGCTGACCCCAGAGAAGATTNTTGAAATGGCGACGATCGATGGGGC 136
      |||||||||||||||||||:|||||
1301 GACGTGCTGACCCCAGAGAAGATTCTTGAAATGGCGACGATCGATGGGGC 1350

      .
135 GCGTTTCGTTGGGGATGGACCACGAGATTGGTTCCATCGAAACCGGCAAG 86
      ||| |||||||||||||||
1351 GCG.TTCGTTGGGAATGGACCACGAGATTGGTTCCATCGAAACCGGCAAG 1399

      .
85 CGCGCGGACCTTATCCTGCTTGACCTGCGTCACCCTCAGACGACTCCTCA 36
      |||||||||||||||
1400 CGCGCGGACCTTATCCTGCTTGACCTGCGTCA.CCTCAGACGACTC..TC 1446

      .
35 CCATCATTGCGGCCACGATCGTGTTTCAGGCTT..... 1
      |||||||||||||||
1447 ACATCATTGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGG 1496

```

*Fig. 5C*

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1 .....CGGCCACGATCGTGTTCAGGCTTACGGCAATGAGGTGGACAC 43  
|||||  
1451 CATTTGGCGGCCACGATCGTGTTCAGGCTTACGGCAATGAGGTGGACAC 1500  
44 TGTCTGATTGACGGAAACGTTGTGATGGAGAACCGCCGCTTGAGCTTTC 93  
|||||  
1501 TGTCTGATTGACGGAAACGTTGTGATGGAGAACCGCCGCTTGAGCTTTC 1550  
94 TTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGCGCC 143  
|||||  
1551 TTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGCGCC 1600  
144 ACAGCTATTTTGCATCGGGCGAAACATGGTGGCTAACCCAGCTTGGCGCA 193  
|||||  
1601 ACAGCTATTTTGCATCGGGCGAAACATGGTGGCTAACCCAGCTTGGCGCA 1649  
194 GCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAATC 243  
|||||  
1650 GCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAATC 1699  
244 GCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGATGG 293  
|||||  
1700 GCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGATGG 1749  
294 ATACAGAATTGCCATGAATGCGGCACTTCCGTCCTTCGCTCGTGTGGAAT 343  
|||||  
1750 ATACAGAATTGCCATGAATGCGGCACTTCCGTCCTTCGCTCGTGTGGAAT 1799  
344 CGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGGTGAA 393  
|||||  
1800 CGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGGTGAA 1849  
394 AGCCCCGAGGATCCTCTAGAGTCCGATTTTCCGATGTCATCACCGGCGCG 443  
|||  
1850 AGCCCCGAG..... 1858  
.  
.

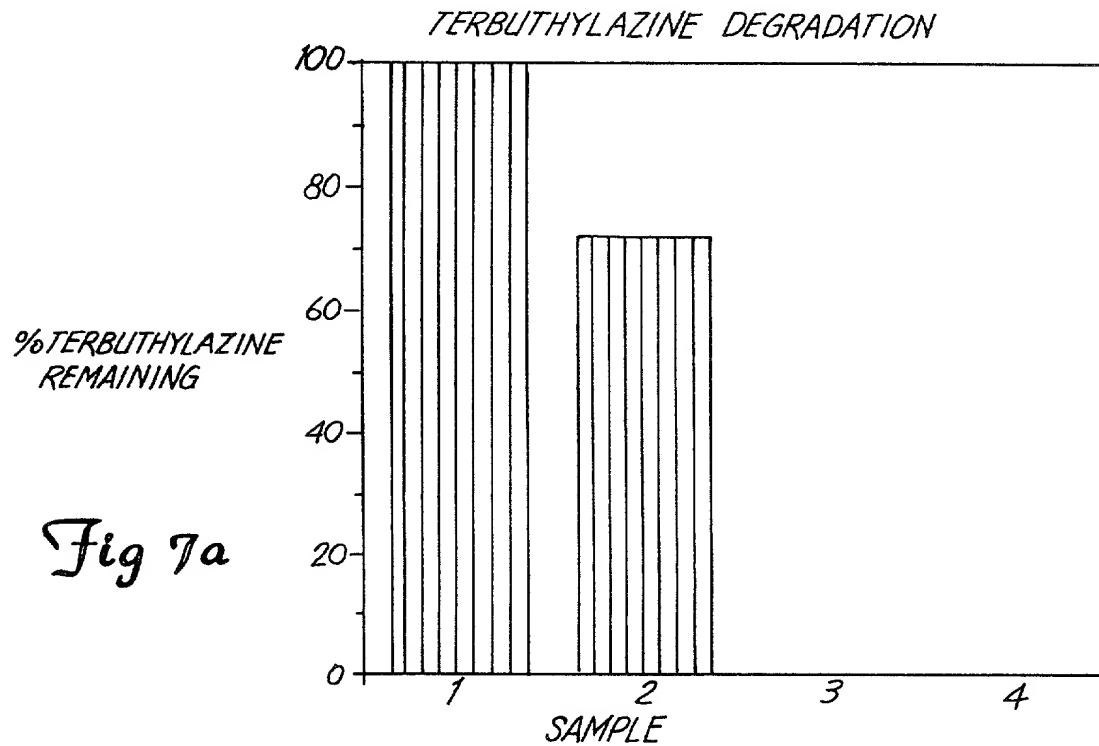
Fig. 5D

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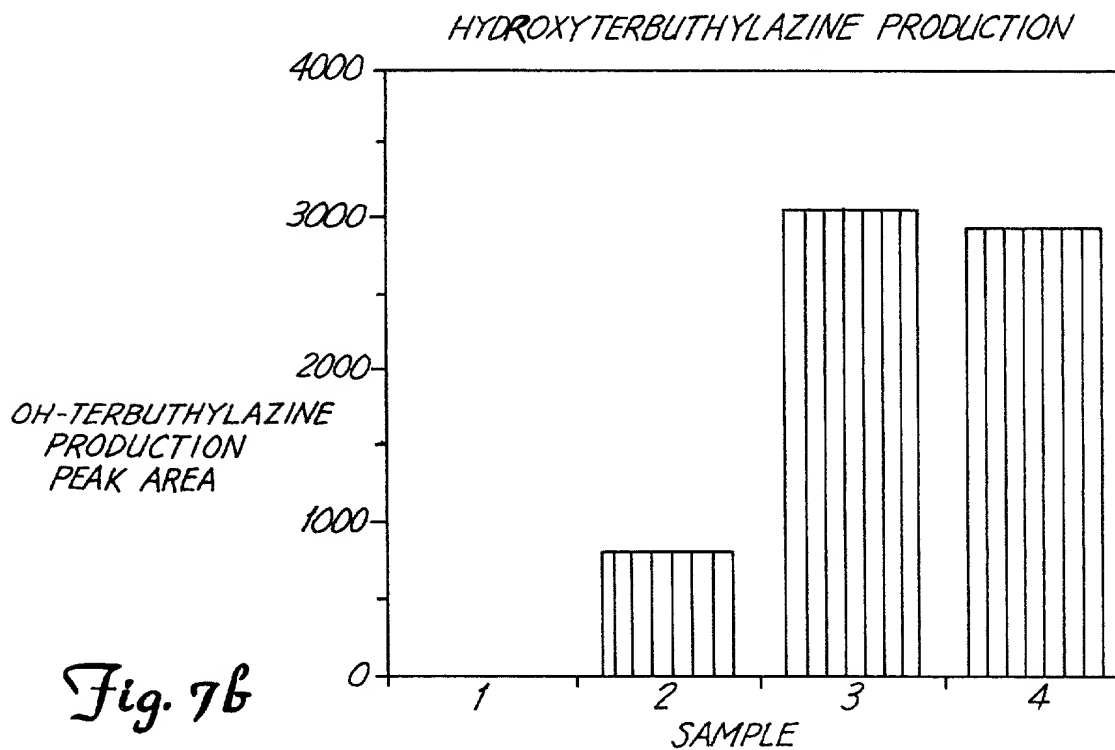
1 ...CCTGCGCGGA.GGCCTCCGCACGGGCGTCAATTCTATGACTGGCTGT 46  
|||  
451 CCTCCTGCGCGGAGGGCCCTCGCACGGACGTCAATTCTATGACTGGCTGT 500  
|||  
47 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTANCG 96  
|||  
501 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTAGCG 550  
|||  
97 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 146  
|||  
551 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 600  
|||  
147 GATCAACGAAAACGCCGATTCCGCCATCTACCCAGGCAACATCGAGGCCG 196  
|||  
601 GATCAACGAAAACGCCGATTCCGCCATCTACCCAGGCAACATCGAGGCCG 650  
|||  
197 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCGCATG 246  
|||  
651 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCGCATG 700  
|||  
247 TTCTTTGATCGGATGGACGGGCGCATTCAGGGTATGTGGACGCCTTGAA 296  
|||  
701 TTCTTTGATCGGATGGACGGGCGCATTCAGGGTATGTGGACGCCTTGAA 750  
|||  
297 GGCTCGCTCTCCCAAGTCGAAGTGTGCTCGATCATGGAGGAAACGGCTG 346  
|||  
751 GGCTCGCTCTCCCAAGTCGAAGTGTGCTCGATCATGGAGGAAACGGCTG 800  
|||  
347 TGGCCAAAGATCGGATCACANCCCTGTCAGATCANTATCATGGCACGGCA 396  
|||  
801 TGGCCAAAGATCGGATCACAGCCCTGTCAGATCAGTATCATGGCACGGCA 850  
|||  
397 NGAGGTCCTATATCANTTTGGCCCGCTCCTGCCACTACCACNGCGGTGAC 446  
|||  
851 GGAGGTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 900  
|||  
447 ATTTNAANGAATTCATNGGCACAA.CCTTCCCCCGTGATCNGGCGGTAA 495  
|||  
901 AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCCGTGATCGGGCGGTAA 950  
|||  
496 TGTNGACCCA..... 505  
|||  
951 TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTCATGGG 1000  
|||

Fig. 6

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*Fig 7a*



*Fig. 7b*

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TERBUTYLAZINE DEGRADATION BY SHUFFLED PROTEINS  
A7, A11 AND T7 - 1 $\mu$ g/ml ptn conc  
- EFFECT OF METAL IONS

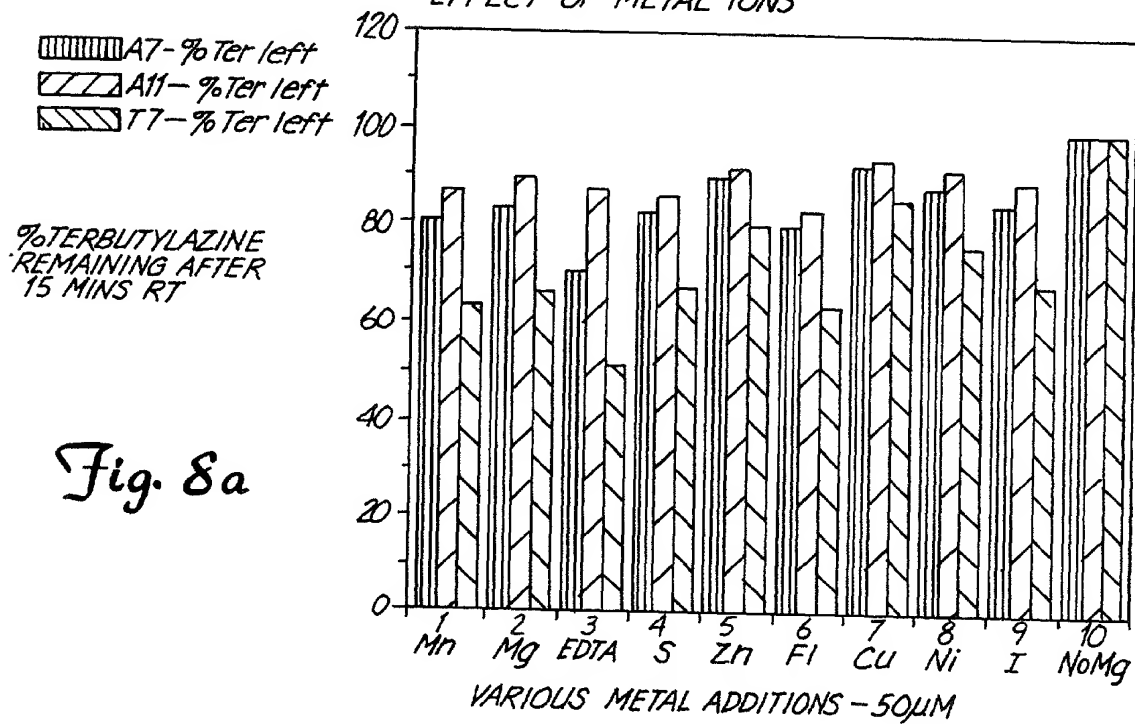


Fig. 8a

## TERBUTYLAZINE DEGRADATION PRODUCT

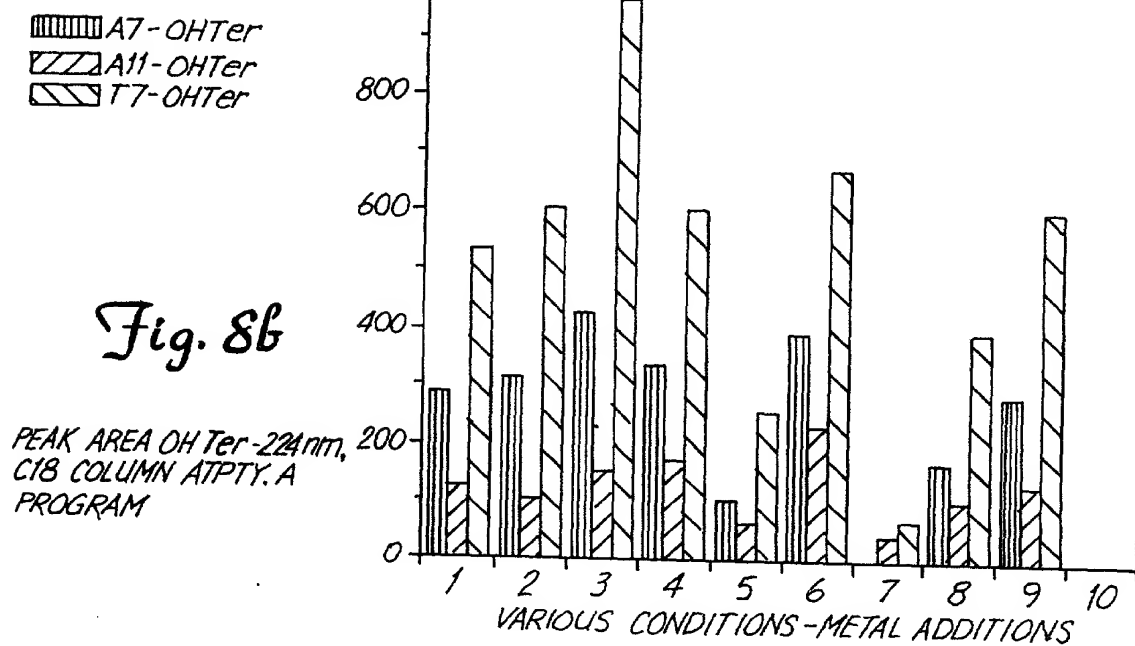


Fig. 8b

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Bacterium      Translation of PCR amplified DNA sequence

	79	92			
ADP	SHGRQ	FYDWLFNVVY	PGQKAMRPED	VAVAVRLYCA	EAVRSGITTI
SG1	<u>PHGRQ</u>	FYDWLFNVLY	PGQKAMRPED	VAVAVRLYCA	EAVRSGITTI
M91-3	SHGRQ	FYDWLFNVLY	PGQKAMRPED	VAVAVRLYCA	EAVRSGITTI
J14a	<u>PHGRQ</u>	FYDWLFNVVY	PGQKAMRPED	VAVAVRLYCA	EAVRSGITTI
38/38	SHGRQ	FYDWLFNVLY	PGQKAMRPED	VAVAVRLYCA	EAVRSGITTI
Clav.	SHGRQ	FYDWLFNVVY	PGQKAMRPED	VAVAVRLYCA	EAVRSGITTI
	125			170	
ADP	NE.NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDALK
SG1	NE.NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDALK
M91-3	NE.NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDTLK
J14a	NE.NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDALK
38/38	NENNADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDTLK
Clav.	NE.NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDALK
ADP	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT
SG1	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT
M91-3	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT
J14a	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT
38/38	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT
CLav.	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT

Fig. 9